SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:
(A) NAME: Deutsches Krebsforschungszentrum Stiftung des öffentlichen Rechts
(B) STREET: Im Neuenheimer Feld 280
(C) CITY: Heidelberg
(E) COUNTRY: Germany
(F) POSTAL CODE: 69120

(ii) TITEL OF INVENTION: DNase active Protein

(iii) NUMBER OF SEQUENCES: 3

(iv) COMPUTER-READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)

(v) CURRENT AAPLICATION DATA:
APPLICATION NUMBER: PCT/DE96/01016

(vi) PRIOR APPLICATION DATA:
(A) APPLICATION DATE: DE 195 21 046.8
(B) APPLICATION DATE: 09-JUN-1995

Cont'd.

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2661 Base pairs
(B) TYPE: Nucleotide
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) TYPE OF MOLEKULE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:795..1700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CTTGAACGCC TGACCTCGTA TCCACCCGCC TCAGCCTCCC AAAGTGCTGG GATTACAGGC 60

ATGAGCCACC ACGCCCAGCC CATAATTTAT TGATTTTTTA AAATTTGTCC AGCCTTCTAT 120

TACCACGTCG AATCCATTAG CTACAGCCAT CCCATGAGAA GCTGAGTGGA TTCAGCCCCA 180

CCTCCTGCTC ACAGACCCTG TCCGAGCACC TCATTTGTCC CAACAGCATT ACTGCAGGAC 240

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CCCCAGGACG TTGGACTGCC AGCTCCCTGG GTCTCCTCCT CTCTGGGGCA GATCCTCAGT      300

CCTCCCTTGA CTTCACGACT GTGGCCAGAT CATGTGTGGA CTGTCCCTCT CTTTGGGTCT      360

CCAGAGCGCT TGCATCAAAC ACCCCTAACT CAGAAGTGTG CAGCCACACT GGGACTCAGA      420

ACCCAACAAC AGGGACAGAA GACTCACGCC CTTGGGGTGC CCGGTCTCGT GGCATCAGGC      480

ATGACTTCCA GCTCCTGCGC CTTCCCCAGC AACTGCTGAC TGGGGACCCA GACCGGGAGC      540

TGAGCGACGG GCCTGGCGAG CGAAGCTCGG GGTCTCACTC AGGCACCAGC CCCTCCTTGC      600

CCCAGGCTTG AGTGACTCAC AGCCCTATTC AGGCAGGAGC TGCTCTTCTG GGGTATCGCG      660

ATCCACTTAA GGATGAGGCA GACTTGGTGA CAAGCTGGTC TGAGCAGCGC TTCCAGAGCC      720

AGAACTGAGC CCAGTGAGAG CGCACCCTGG AGCAGCCTGG ATTCCTGGGG TGTCCCCGGC      780

AGCCACACAC AGCC ATG CAC TAC CCA ACT GCA CTC CTC TTC CTC ATC CTG          830
               Met His Tyr Pro Thr Ala Leu Leu Phe Leu Ile Leu
                 1               5                  10

GCC AAT GGG GCC CAG GCC TTT CGC ATC TGC GCC TTC AAT GCC CAG CGG          878
Ala Asn Gly Ala Gln Ala Phe Arg Ile Cys Ala Phe Asn Ala Gln Arg
         15                  20                  25

CTG ACA CTG GCC AAG GTG GCC AGG GAG CAG GTG ATG GAC ACC TTA GTT          926
Leu Thr Leu Ala Lys Val Ala Arg Glu Gln Val Met Asp Thr Leu Val
     30                  35                  40

CGG ATA CTG GCT CGC TGT GAC ATC ATG GTG CTG CAG GAG GTG GTA GAC          974
Arg Ile Leu Ala Arg Cys Asp Ile Met Val Leu Gln Glu Val Val Asp
 45                  50                  55                  60

TCT TCC GGC AGC GCC ATC CCC CTC CTG CTT CGA GAA CTC AAT CGA TTT         1022
Ser Ser Gly Ser Ala Ile Pro Leu Leu Leu Arg Glu Leu Asn Arg Phe
                 65                  70                  75

GAT GGC TCT GGG CCC TAC AGC ACC CTG AGC AGC CCC CAG CTG GGG CGC         1070
Asp Gly Ser Gly Pro Tyr Ser Thr Leu Ser Ser Pro Gln Leu Gly Arg
             80                  85                  90

AGC ACC TAC ATG GAG ACG TAT GTG TAC TTC TAT CGG TCA CAC AAA ACA         1118
Ser Thr Tyr Met Glu Thr Tyr Val Tyr Phe Tyr Arg Ser His Lys Thr
         95                  100                 105

CAG GTC CTG AGT TCC TAC GTG TAC AAC GAT GAG GAT GAC GTC TTT GCC         1166
Gln Val Leu Ser Ser Tyr Val Tyr Asn Asp Glu Asp Asp Val Phe Ala
    110                 115                 120

CGG GAG CCA TTT GTG GCC CAG TTC TCT TTG CCC AGC AAT GTC CTT CCC         1214
Arg Glu Pro Phe Val Ala Gln Phe Ser Leu Pro Ser Asn Val Leu Pro
125                 130                 135                 140

AGC CTG GTG TTG GTC CCG CTG CAC ACC ACT CCT AAG GCC GTA GAG AAG         1262
Ser Leu Val Leu Val Pro Leu His Thr Thr Pro Lys Ala Val Glu Lys
                145                 150                 155
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GAG CTG AAC GCC CTC TAC GAT GTG TTT CTG GAG GTC TCC CAG CAC TGG      1310
Glu Leu Asn Ala Leu Tyr Asp Val Phe Leu Glu Val Ser Gln His Trp
            160                 165                 170

CAG AGC AAG GAC GTG ATC CTG CTT GGG GAC TTC AAT GCT GAC TGC GCT      1358
Gln Ser Lys Asp Val Ile Leu Leu Gly Asp Phe Asn Ala Asp Cys Ala
        175                 180                 185

TCA CTG ACC AAA AAG CGC CTG GAC AAG CTG GAG CTG CGG ACT GAG CCA      1406
Ser Leu Thr Lys Lys Arg Leu Asp Lys Leu Glu Leu Arg Thr Glu Pro
    190                 195                 200

GGC TTC CAC TGG GTG ATT GCC GAT GGG GAG GAC ACC ACA GTG CGG GCC      1454
Gly Phe His Trp Val Ile Ala Asp Gly Glu Asp Thr Thr Val Arg Ala
205                 210                 215                 220

AGC ACC CAC TGC ACC TAT GAC CGC GTC GTG CTG CAC GGG GAG CGC TGC      1502
Ser Thr His Cys Thr Tyr Asp Arg Val Val Leu His Gly Glu Arg Cys
                225                 230                 235

CGG AGT CTG CTG CAC ACT GCG GCT GCC TTT GAC TTC CCC ACG AGC TTC      1550
Arg Ser Leu Leu His Thr Ala Ala Ala Phe Asp Phe Pro Thr Ser Phe
            240                 245                 250

CAG CTC ACC GAG GAG GAG GCC CTC AAC ATC AGT GAC CAC TAC CCC GTG      1598
Gln Leu Thr Glu Glu Glu Ala Leu Asn Ile Ser Asp His Tyr Pro Val
        255                 260                 265

GAG GTG GAG CTG AAG CTG AGC CAG GCG CAC AGC GTC CAG CCT CTC AGC      1646
Glu Val Glu Leu Lys Leu Ser Gln Ala His Ser Val Gln Pro Leu Ser
    270                 275                 280

CTC ACT GTT CTG TTG CTG CTA TCA CTC CTG TCC CCT CAG CTG TGC CCT      1694
Leu Thr Val Leu Leu Leu Leu Ser Leu Leu Ser Pro Gln Leu Cys Pro
285                 290                 295                 300

GCT GCC TGAGCGTCCC CCTACCCCCC CAGGGCCTGC TGCCTTTTGG GACTTAAACC      1750
Ala Ala

CCAGCCTCCC CCGTCCATCC AGCCCTGGGG CTGGGGGGCT TCAACTATAG TTGCCCTGTG    1810

ACTGTAGTCC ACCCCTGCCT GCCTTGTTTG ATTTGGCTCT TGTTCTTTGG TTGGGCTTGT    1870

GCCTAGATTA GGAGAGGAAG CCAGGGGCCC TGCACTCATG CCACCTGCCA GGTAGTGTAG    1930

TATCAGGAGT GGAGACAAAG TGGGCTCTGG GTTGGGGTAG GGGAAGGGAG GGTTCAGAAA    1990

GAGGAATGAA GATGTTGTAT GACAAGAAGG AAAGTTACTG AGAACAAAAA CCCAGATTGG    2050

TGAGATAGGA CACTTGTGCA GCAGATATGC CAATGGGCCA TGTTTATTGT GGATGGGTAA    2110

GAATCACCAG GAAACCATTA AGCCCCAATA GCTACAAGGA GGGTGGTTAA TCTGCTATAT    2170

CAAACTCCTT CCCTGAAACC AGCAAACACC GGGAAACATT TTGGCTCATT ATAATCCGGT    2230

GAACAATGCA GTCAGGCCTG TTATAACCGC TGAGCAGCCA CACTCGCACC TCCTGGGTGC    2290
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TGTAGTCTGT GTTGGTACAG GCTTCTGCAT GCCTGGTAAA GTCCAGCCAA GGCTGGTCAA 2350

GGCAACATCT CCACACAGAA AATCTGCACC AGTTATGTAA GCTAAAAAGC TGTGTGAACC 2410

CAGGTGTCCC GGAAAGGGGC TGCAGGACAC AGCAAAATGC CAGCAGCGTG CCGGACCCCT 2470

CCCTTCCATC CTCCTCTCCA AAGAACAGAG GTCAGGAAAA ACACTGGCTG GGACGCTAGA 2530

AGGGTCATGT GTTAACTATA ATCACATTTA TGGTTTGGAA CCATCACCCC AAGGTAAAAA 2590

AAAAAATAAA AGGTATGTTT GGCAAAATAA AATAAAGGTA ATTAAAAACC TAAAAAAAAA 2650

AAAAAAAAAA A 2661

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 Base pairs
(B) TYPE: Nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: other nucleic acid
(A) DESCRIPTION: /desc = "DNA-Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

CAGGGATCCG ATGACGATGA CAAAATGCAC TACCCAACTG CAC 43

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 Base pairs
(B) TYPE: Nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: other nucleic acid
(A) DESCRIPTION: /desc = "DNA-Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GGGGGATCCT CAGGCAGCAG GGCACAG 27